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<110> TAKASHIMA, SHOU
TSUJIMOTO, MASAFUMI
TSUJI, SHUICHI

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ccg gat tac aac ctg ttc act cca tat att cag cat cgt cag aga aac Pro Asp Tyr Asn Leu Phe Thr Pro Tyr Ile Gln His Arg Gln Arg Asn 390 395 400	1378
cca aat cag cca ttt tac att ctt cat cct aaa ttt ata tgg cag ctc Pro Asn Gln Pro Phe Tyr Ile Leu His Pro Lys Phe Ile Trp Gln Leu 405 410 415	1426
tgg gat att atc cag gag aac act aaa gag aag att caa cca aac cca Trp Asp Ile Ile Gln Glu Asn Thr Lys Glu Lys Ile Gln Pro Asn Pro 420 425 430	1474
cca tct tct ggt ttc att gga atc ctc atc atg atg tcc atg tgc aga Pro Ser Ser Gly Phe Ile Gly Ile Leu Ile Met Met Ser Met Cys Arg 435 440 445	1522
gag gtg cac gtg tat gaa tat atc cca tcc gtg cgg cag acg gag ctg Glu Val His Val Tyr Glu Tyr Ile Pro Ser Val Arg Gln Thr Glu Leu 450 455 460 465	1570
tgc cac tac cac gag .ctg tac tac gac gca gcc tgc acc ctc ggg gcg Cys His Tyr His Glu Leu Tyr Tyr Asp Ala Ala Cys Thr Leu Gly Ala 470 475 480	1618

tac cac cca cta ctc tat gag aag ctc ctg gtg cag cgc ctg aac atg 1666
 Tyr His Pro Leu Leu Tyr Glu Lys Leu Leu Val Gln Arg Leu Asn Met
 485 490 495

 ggc acg cag ggg gat ttg cat cgc aag ggc aag gtg gtt ctt cct ggc 1714
 Gly Thr Gln Gly Asp Leu His Arg Lys Gly Lys Val Val Leu Pro Gly
 500 505 510

 ttc cag gcg gtg cac tgc cct gca cca agt cca gtc att cca cac tct 1762
 Phe Gln Ala Val His Cys Pro Ala Pro Ser Pro Val Ile Pro His Ser
 515 520 525

 taaaaagggt ttcttggaa tcaatgtgca atggtaca 1800

<210> 7
 <211> 524
 <212> PRT
 <213> Mus sp.

<400> 7
 Met Lys Pro His Leu Lys Gln Trp Arg Gln Arg Met Leu Phe Gly Ile
 1 5 10 15

 Phe Val Trp Gly Leu Leu Phe Leu Ala Ile Phe Ile Tyr Phe Thr Asn
 20 25 30

 Ser Asn Pro Ala Ala Pro Met Pro Ser Ser Phe Ser Phe Leu Glu Ser
 35 40 45

 Arg Gly Leu Leu Pro Leu Gln Gly Lys Gln Arg Val Ile Met Gly Ala
 50 55 60

 Leu Gln Glu Pro Ser Leu Pro Arg Ser Leu Asp Ala Ser Lys Val Leu
 65 70 75 80

 Leu Asp Ser His Pro Glu Asn Pro Phe His Pro Trp Pro Gly Asp Pro
 85 90 95

 Gln Lys Trp Asp Gln Ala Pro Asn Gly Phe Asp Asn Gly Asp Glu Phe
 100 105 110

 Phe Thr Ser Gln Val Gly Arg Lys Ser Gln Ser Ala Phe Tyr Pro Glu
 115 120 125

 Glu Asp Ser Tyr Phe Phe Val Ala Asp Gln Pro Glu Leu Tyr His His
 130 135 140

 Arg Gln Gly Ala Leu Glu Leu Pro Ser Pro Gly Glu Thr Ser Trp Arg
 145 150 155 160

 Ser Gly Pro Val Gln Pro Lys Gln Lys Leu Leu His Pro Arg Arg Gly
 165 170 175

 Ser Leu Pro Glu Glu Ala Tyr Asp Ser Asp Met Leu Ser Ala Ser Met
 180 185 190

Ser Arg Ala Phe Leu Tyr Arg Leu Trp Lys Gly Ala Val Ser Ser Lys
 195 200 205

Met Leu Asn Pro Arg Leu Gln Lys Ala Met Arg Tyr Tyr Met Ser Phe
 210 215 220

Asn Lys His Gly Val Arg Phe Arg Arg Gly Arg Arg Glu Ala Thr
 225 230 235 240

Arg Thr Gly Pro Glu Leu Leu Cys Glu Met Arg Arg Arg Val Arg Val
 245 250 255

Arg Thr Leu Asp Gly Arg Glu Ala Pro Phe Ser Gly Leu Gly Trp Arg
 260 265 270

Pro Leu Val Pro Gly Val Pro Leu Ser Gln Leu His Pro Arg Gly Leu
 275 280 285

Ser Ser Cys Ala Val Val Met Ser Ala Gly Ala Ile Leu Asn Ser Ser
 290 295 300

Leu Gly Glu Glu Ile Asp Ser His Asp Ala Val Leu Arg Phe Asn Ser
 305 310 315 320

Ala Pro Thr Arg Gly Tyr Glu Lys Asp Val Gly Asn Lys Thr Thr Val
 325 330 335

Arg Ile Ile Asn Ser Gln Ile Leu Ala Asn Pro Ser His His Phe Ile
 340 345 350

Asp Ser Ala Leu Tyr Lys Asp Val Ile Leu Val Ala Trp Asp Pro Ala
 355 360 365

Pro Tyr Ser Ala Asn Leu Asn Leu Trp Tyr Lys Lys Pro Asp Tyr Asn
 370 375 380

Leu Phe Thr Pro Tyr Ile Gln His Arg Arg Lys Tyr Pro Thr Gln Pro
 385 390 395 400

Phe Tyr Ile Leu His Pro Lys Phe Ile Trp Gln Leu Trp Asp Ile Ile
 405 410 415

Gln Glu Asn Thr Arg Glu Lys Ile Gln Pro Asn Pro Pro Ser Ser Gly
 420 425 430

Phe Ile Gly Ile Leu Ile Met Met Ser Met Cys Lys Glu Val His Val
 435 440 445

Tyr Glu Tyr Ile Pro Ser Val Arg Gln Thr Glu Leu Cys His Tyr His
 450 455 460

Glu Leu Tyr Tyr Asp Ala Ala Cys Thr Leu Gly Ala Tyr His Pro Leu
 465 470 475 480

Leu Tyr Glu Lys Leu Leu Val Gln Arg Leu Asn Thr Gly Thr Gln Ala
 485 490 495

Asp Leu His His Lys Gly Lys Val Val Leu Pro Gly Phe Gln Thr Leu
 500 505 510

Arg Cys Pro Val Thr Ser Pro Asn Asn Thr His Ser
 515 520

<210> 8
 <211> 1611
 <212> DNA
 <213> Mus sp.

<220>
 <221> CDS
 <222> (3)...(1574)

<400> 8
 ca atg aaa cca cac ttg aag caa tgg cga caa cga atg ctc ttt gga 47
 Met Lys Pro His Leu Lys Gln Trp Arg Gln Arg Met Leu Phe Gly
 1 5 10 15

ata ttt gtt tgg ggg ctc ctc ttt ttg gca att ttc atc tac ttc acc 95
 Ile Phe Val Trp Gly Leu Leu Phe Leu Ala Ile Phe Ile Tyr Phe Thr
 20 25 30

aac agc aat cct gcg gca cct atg ccc agc tcc ttt tcc ttc ctg gag 143
 Asn Ser Asn Pro Ala Ala Pro Met Pro Ser Ser Phe Ser Phe Leu Glu
 35 40 45

agc cgt ggg ctc ctg cct cta cag ggc aag cag cgg gtc atc atg ggc 191
 Ser Arg Gly Leu Leu Pro Leu Gln Gly Lys Gln Arg Val Ile Met Gly
 50 55 60

gct ttg cag gaa ccc tct ttg ccc aga agt ttg gat gca agc aaa gtg 239
 Ala Leu Gln Glu Pro Ser Leu Pro Arg Ser Leu Asp Ala Ser Lys Val
 65 70 75

ctt ctg gac agc cac cct gag aac cct ttc cac cct tgg cct ggg gac 287
 Leu Leu Asp Ser His Pro Glu Asn Pro Phe His Pro Trp Pro Gly Asp
 80 85 90 95

cca cag aaa tgg gat cag gcc cca aat ggc ttt gac aat ggg gat gag 335
 Pro Gln Lys Trp Asp Gln Ala Pro Asn Gly Phe Asp Asn Gly Asp Glu
 100 105 110

ttt ttt aca tcc cag gtt ggg agg aaa tca caa agc gct ttc tat ccc 383
 Phe Phe Thr Ser Gln Val Gly Arg Lys Ser Gln Ser Ala Phe Tyr Pro
 115 120 125

gag gaa gat agc tat ttt ttt gtt gcg gat cag cct gag ttg tac cac 431
 Glu Glu Asp Ser Tyr Phe Phe Val Ala Asp Gln Pro Glu Leu Tyr His
 130 135 140

cac agg cag ggt gca ctg gag ctg cca tct cca ggg gag aca tca tgg 479
 His Arg Gln Gly Ala Leu Glu Leu Pro Ser Pro Gly Glu Thr Ser Trp
 145 150 155

cga tca gga cct gtt cag ccc aag cag aag ctg ctt cac cca agg cga Arg Ser Gly Pro Val Gln Pro Lys Gln Lys Leu Leu His Pro Arg Arg	527
160 165 170 175	
ggc agc ttg cct gag gaa gcc tat gac agc gac atg ctg tca gcc tcc Gly Ser Leu Pro Glu Glu Ala Tyr Asp Ser Asp Met Leu Ser Ala Ser	575
180 185 190	
atg tcg aga gcc ttc ctg tac cgg ctc tgg aag ggg gcc gtg tcc tct Met Ser Arg Ala Phe Leu Tyr Arg Leu Trp Lys Gly Ala Val Ser Ser	623
195 200 205	
aag atg ttg aac ccg cgc ctg cag aag gcc atg cgt tac tac atg tcc Lys Met Leu Asn Pro Arg Leu Gln Lys Ala Met Arg Tyr Tyr Met Ser	671
210 215 220	
ttc aac aag cat ggt gtg cgc ttc cgc agg cgg ggt cgg cgt gaa gct Phe Asn Lys His Gly Val Arg Phe Arg Arg Arg Gly Arg Arg Glu Ala	719
225 230 235	
aca cgt aca ggg ccg gag ctg ctg tgt gag atg cgc aga cgt gtg cgt Thr Arg Thr Gly Pro Glu Leu Leu Cys Glu Met Arg Arg Arg Val Arg	767
240 245 250 255	
gtg cgc acg ttg gac ggc aga gag gcg ccc ttc tcg ggg ctg ggc tgg Val Arg Thr Leu Asp Gly Arg Glu Ala Pro Phe Ser Gly Leu Gly Trp	815
260 265 270	
cgg cct ctg gta cca ggt gta cct ctg agc cag ttg cac ccg cgc ggt Arg Pro Leu Val Pro Gly Val Pro Leu Ser Gln Leu His Pro Arg Gly	863
275 280 285	
ctg agc agc tgc gca gtt gtc atg tct gtc ggt gcc atc ctg aac tcc Leu Ser Cys Ala Val Val Met Ser Ala Gly Ala Ile Leu Asn Ser	911
290 295 300	
tcc ttg ggg gag gaa atc gat tct cat gat gca gtt ttg aga ttt aac Ser Leu Gly Glu Ile Asp Ser His Asp Ala Val Leu Arg Phe Asn	959
305 310 315	
tct gcc cct acc cgt ggc tac gag aaa gat gtc gga aat aaa acc aca Ser Ala Pro Thr Arg Gly Tyr Glu Lys Asp Val Gly Asn Lys Thr Thr	1007
320 325 330 335	
gta cgc atc att aat tct cag att ctg gcc aac ccc agc cat cac ttc Val Arg Ile Ile Asn Ser Gln Ile Leu Ala Asn Pro Ser His His Phe	1055
340 345 350	
att gac agt gct tta tat aaa gat gtt atc ctg gta gcc tgg gat cct Ile Asp Ser Ala Leu Tyr Lys Asp Val Ile Leu Val Ala Trp Asp Pro	1103
355 360 365	
gct cct tat tct gcc aat ctt aac ctg tgg tat aag aag cca gat tac Ala Pro Tyr Ser Ala Asn Leu Asn Leu Trp Tyr Lys Lys Pro Asp Tyr	1151
370 375 380	

aac ctt ttc act cca tat atc cag cat cgc cgg aaa tac ccg act cag	1199
Asn Leu Phe Thr Pro Tyr Ile Gln His Arg Arg Lys Tyr Pro Thr Gln	
385 390 395	
cca ttt tac att ctt cac ccc aag ttc ata tgg cag ctt tgg gac att	1247
Pro Phe Tyr Ile Leu His Pro Lys Phe Ile Trp Gln Leu Trp Asp Ile	
400 405 410 415	
atc cag gag aat aca agg gag aag ata cag ccc aac cca cca tct tct	1295
Ile Gln Glu Asn Thr Arg Glu Lys Ile Gln Pro Asn Pro Pro Ser Ser	
420 425 430	
ggg ttt att gga atc ctc atc atg atg tcc atg tgt aaa gag gtg cac	1343
Gly Phe Ile Gly Ile Leu Ile Met Met Ser Met Cys Lys Glu Val His	
435 440 445	
gtg tat gag tac atc cca tct gtt cga cag aca gag ctt tgc cac tac	1391
Val Tyr Glu Tyr Ile Pro Ser Val Arg Gln Thr Glu Leu Cys His Tyr	
450 455 460	
cat gag ctg tac tac gac gca gcc tgc acc ttg ggg gcc tac cac cca	1439
His Glu Leu Tyr Tyr Asp Ala Ala Cys Thr Leu Gly Ala Tyr His Pro	
465 470 475	
ctg ctc tat gaa aag cta ctg gtg cag cgc ctt aac aca ggc acc cag	1487
Leu Leu Tyr Glu Lys Leu Leu Val Gln Arg Leu Asn Thr Gly Thr Gln	
480 485 490 495	
gca gac ttg cat cac aag ggc aag gta gtc ttg cca ggc ttc cag acc	1535
Ala Asp Leu His His Lys Gly Lys Val Val Leu Pro Gly Phe Gln Thr	
500 505 510	
ctt cgg tgt cca gta acc agc ccc aac aat aca cat tct taaaatggaa	1584
Leu Arg Cys Pro Val Thr Ser Pro Asn Asn Thr His Ser	
515 520	
ctcttgggaa ctgatgtgca ataagg	1611

<210> 9
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 9
cttttctgga gaactaaagg

20

<210> 10
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 10
aattgcagtt tgaggattcc

20

<210> 11
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 11
tggctcagga tgagatcggg

20

<210> 12
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 12
tactagcgct ccctgtgatt gg

22

<210> 13
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 13
tgctctcgag cccagccgac gcgcctgcc

30

<210> 14
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 14
tattctcgag ctaagaaaacg ttaagccgtt

30

<210> 15
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 15
caattgacat atctgaatga gaagtcgctc 30

<210> 16
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 16
tactaacatc tcctgtggtt gg 22

<210> 17
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 17
ccagtgtccc agccttttgt 20

<210> 18
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 18
tgagtgggga agctttggtc 20

<210> 19
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 19
gacaatgggg atgagtttt tacatccag 30

<210> 20
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 20
cgatttcctc ccccaaggag gagttcagg 29

<210> 21
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 21
acgttggacg gcagagaggc gcccttctcg 30

<210> 22
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 22
accttattgc acatcagttc ccaagagttc 30

<210> 23
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 23
caatgaaacc acacttgaag caatggcgac 30

<210> 24
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 24
cgcaacaaaa aaatagctat cttcctcggg 30

<210> 25
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 25
tcatctactt cacctcgagc aaccccgctg 30

<210> 26
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 26
catccaattg accaacagca atcctgcggc 30

<210> 27
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 27
ttatgattca caccaacctg aag 23

<210> 28
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 28
ctttgtactt gttcatgctt agg

23

<210> 29
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 29
agacgtcatt ttgggtggcct ggg

23

<210> 30
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 30
ttaagagtgt ggaatgactg g

21

<210> 31
<211> 355
<212> PRT
<213> Mus sp.

<400> 31
Met Ser Pro Cys Gly Arg Ala Leu His Thr Ser Arg Gly Ala Met Ala
1 5 10 15

Met Leu Ala Arg Lys Phe Pro Arg Thr Arg Leu Pro Val Gly Ala Ser
20 25 30

Ala Leu Cys Val Val Leu Cys Trp Leu Tyr Ile Phe Pro Val Tyr
35 40 45

Arg Leu Pro Asn Glu Lys Glu Ile Val Gln Gly Val Leu Ala Gln Arg
50 55 60

Thr Ala Trp Arg Thr Asn Gln Thr Ser Ala Ser Leu Phe Arg Arg Gln
 65 70 75 80
 Met Glu Asp Cys Cys Asp Pro Ala His Leu Phe Ala Met Thr Lys Met
 85 90 95
 Asn Ser Pro Met Gly Lys Ser Leu Trp Tyr Asp Gly Glu Leu Leu Tyr
 100 105 110
 Ser Phe Thr Ile Asp Asn Ser Thr Tyr Ser Leu Phe Pro Gln Ala Thr
 115 120 125
 Pro Phe Gln Leu Pro Leu Lys Lys Cys Ala Val Val Gly Asn Gly Gly
 130 135 140
 Ile Leu Lys Met Ser Gly Cys Ala Arg Gln Ile Asp Glu Pro Asn Phe
 145 150 155 160
 Val Met Arg Cys Asn Leu Pro Pro Leu Ser Ser Glu Tyr Thr Arg Asp
 165 170 175
 Val Gly Ser Lys Thr Gln Leu Val Thr Ala Asn Pro Ser Ile Ile Arg
 180 185 190
 Gln Arg Phe Glu Asn Leu Leu Trp Ser Arg Lys Lys Phe Val Asp Asn
 195 200 205
 Met Lys Ile Tyr Asn His Ser Tyr Ile Tyr Met Pro Ala Phe Ser Met
 210 215 220
 Lys Thr Gly Thr Glu Pro Ser Leu Arg Val Tyr Tyr Thr Leu Lys Asp
 225 230 235 240
 Val Gly Ala Asn Gln Thr Val Leu Phe Ala Asn Pro Asn Phe Leu Arg
 245 250 255
 Asn Ile Gly Lys Phe Trp Lys Ser Arg Gly Ile His Ala Lys Arg Leu
 260 265 270
 Ser Thr Gly Leu Phe Leu Val Ser Ala Ala Leu Gly Leu Cys Glu Glu
 275 280 285
 Val Ser Ile Tyr Gly Phe Trp Pro Phe Ser Val Asn Met Gln Gly Asp
 290 295 300
 Pro Ile Ser His His Tyr Tyr Asp Asn Val Leu Pro Phe Ser Gly Tyr
 305 310 315 320
 His Ala Met Pro Glu Glu Phe Leu Gln Leu Trp Tyr Leu His Lys Ile
 325 330 335
 Gly Ala Leu Arg Met Gln Leu Asp Pro Cys Glu Glu Pro Ser Pro Gln
 340 345 350
 Pro Thr Ser
 355

<210> 32
<211> 412
<212> PRT
<213> Mus sp.

<400> 32
Met Arg Tyr Ala Asp Pro Ser Ala Asn Arg Asp Leu Leu Gly Asn Arg
1 5 10 15
Thr Leu Leu Phe Ile Phe Ile Cys Ala Phe Ala Leu Val Thr Leu Leu
20 25 30
Gln Gln Ile Leu Tyr Ser Lys Ser Tyr Ile Lys Arg Gly Phe Gln Phe
35 40 45
Gly Trp Gln Arg Gly Asp Gln Gln Ala Asn Trp Thr Gly Leu Phe Asn
50 55 60
Asp Ser Asp Ser Pro Thr Glu Gln Asn Ile Thr Gly Ser Ser Ser Arg
65 70 75 80
Tyr Phe Glu Phe Tyr Lys Glu Pro Leu Glu Phe Asn Ser Thr Arg Cys
85 90 95
Leu Glu Leu Arg Gln Glu Ile Leu Glu Val Lys Val Leu Ser Met Val
100 105 110
Lys Gln Ser Glu Leu Phe Glu Arg Trp Lys Ser Leu Gln Ile Cys Lys
115 120 125
Trp Ala Met Gly Ala Ser Glu Ala Ser Leu Phe Lys Ser Thr Leu Ser
130 135 140
Arg Cys Cys Asn Ala Pro Asn Phe Leu Phe Thr Thr Gln Lys Asn Thr
145 150 155 160
Pro Val Glu Thr Asn Leu Arg Tyr Glu Val Glu Ser Ser Gly Leu Tyr
165 170 175
His Ile Asp Gln Glu Ile Phe Lys Met Phe Pro Lys Glu Met Pro Tyr
180 185 190
Tyr Arg Ser Gln Phe Lys Lys Cys Ala Val Val Gly Asn Gly Gly Ile
195 200 205
Leu Lys Asn Ser Gly Cys Gly Lys Glu Ile Asn Ser Ala Asp Phe Val
210 215 220
Phe Arg Cys Asn Leu Pro Pro Ile Ser Gly Ile Tyr Thr Thr Asp Val
225 230 235 240
Gly Glu Lys Thr Asp Val Val Thr Val Asn Pro Ser Ile Ile Ile Asp
245 250 255
Arg Phe His Lys Leu Glu Lys Trp Arg Arg Pro Phe Phe Ser Val Leu
260 265 270

Gln Arg Tyr Glu Asn Ala Ser Val Leu Leu Pro Ala Phe Tyr Asn Val
 275 280 285

Arg Asn Thr Leu Val Ser Phe Arg Val Lys Tyr Met Leu Asp Asp Phe
 290 295 300

Gln Ser Arg Gln Pro Val Tyr Phe Phe His Pro Gln Tyr Leu Ser Ser
 305 310 315 320

Val Ser Arg Tyr Trp Leu Ser Leu Gly Val Arg Ala Arg Arg Ile Ser
 325 330 335

Thr Gly Leu Ser Leu Val Thr Ala Ala Leu Glu Leu Cys Glu Glu Val
 340 345 350

His Leu Phe Gly Phe Trp Ala Phe Pro Met Asn Pro Ser Gly Phe Phe
 355 360 365

Ile Thr His His Tyr Tyr Asp Asn Val Lys Pro Lys Pro Gly Phe His
 370 375 380

Ala Met Pro Ser Glu Ile Phe Thr Phe Leu Arg Met His Ser Arg Gly
 385 390 395 400

Ile Leu Arg Val His Thr Gly Thr Cys Asn Cys Cys
 405 410

<210> 33
 <211> 200
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (3)..(173)

<400> 33
 tt cat cct aaa ttt ata tgg cag ctc tgg gat att atc cag gag aac 47
 His Pro Lys Phe Ile Trp Gln Leu Trp Asp Ile Ile Gln Glu Asn
 1 5 10 15

act aaa gag aag att caa cca aac cca cca tct tct ggt ttc att ggc 95
 Thr Lys Glu Lys Ile Gln Pro Asn Pro Pro Ser Ser Gly Phe Ile Gly
 20 25 30

tca ttt gta aaa att ggc cat atc aga gct tgc agt gag ccg aga tca 143
 Ser Phe Val Lys Ile Gly His Ile Arg Ala Cys Ser Glu Pro Arg Ser
 35 40 45

cgc gac tgc act cca gcc tgg acg aca gag tgagactcca tctaaaaaaa 193
 Arg Asp Cys Thr Pro Ala Trp Thr Thr Glu
 50 55

aaaaaaaa 200

<210> 34

<211> 57

<212> PRT

<213> Homo sapiens

<400> 34

His	Pro	Lys	Phe	Ile	Trp	Gln	Leu	Trp	Asp	Ile	Ile	Gln	Glu	Asn	Thr
1															15

Lys	Glu	Lys	Ile	Gln	Pro	Asn	Pro	Pro	Ser	Ser	Gly	Phe	Ile	Gly	Ser
															30
			20					25							

Phe	Val	Lys	Ile	Gly	His	Ile	Arg	Ala	Cys	Ser	Glu	Pro	Arg	Ser	Arg
															45
			35				40								

Asp	Cys	Thr	Pro	Ala	Trp	Thr	Thr	Glu							
															55
			50												

<210> 35

<211> 406

<212> PRT

<213> Homo sapiens

<400> 35

Met	Ile	His	Thr	Asn	Leu	Lys	Lys	Phe	Ser	Cys	Cys	Val	Leu	Val	
1															15

Phe	Leu	Leu	Phe	Ala	Val	Ile	Cys	Val	Trp	Lys	Glu	Lys	Lys	Gly
														30
			20					25						

Ser	Tyr	Tyr	Asp	Ser	Phe	Lys	Leu	Gln	Thr	Lys	Glu	Phe	Gln	Val	Leu
															45
			35				40								

Lys	Ser	Leu	Gly	Lys	Leu	Ala	Met	Gly	Ser	Asp	Ser	Gln	Ser	Val	Ser
															60
			50			55									

Ser	Ser	Ser	Thr	Gln	Asp	Pro	His	Arg	Gly	Arg	Gln	Ala	Leu	Gly	Ser
															80
			65			70			75						

Leu	Arg	Asp	Ile	Pro	Lys	Ala	Lys	Pro	Glu	Ala	Ser	Phe	Gln	Val	Trp
															95
			85					90							

Asn	Lys	Asp	Ser	Ser	Ser	Lys	Asn	Leu	Ile	Pro	Arg	Leu	Gln	Lys	Ile
															110
			100					105							

Trp	Lys	Asn	Tyr	Leu	Ser	Met	Asn	Lys	Tyr	Lys	Val	Ser	Tyr	Lys	Gly
															125
			115					120							

Pro	Gly	Pro	Gly	Ile	Lys	Phe	Ser	Ala	Glu	Ala	Leu	Arg	Cys	His	Leu
															140
			130			135									

Arg	Asp	His	Val	Asn	Val	Ser	Met	Val	Glu	Val	Thr	Asp	Phe	Pro	Phe
															160
			145			150				155					

Asn	Thr	Ser	Glu	Trp	Glu	Gly	Tyr	Leu	Pro	Lys	Glu	Ser	Ile	Arg	Thr
															175
			165					170							

Lys Ala Gly Pro Trp Gly Arg Cys Ala Val Val Ser Ser Ala Gly Ser
 180 185 190

 Leu Lys Ser Ser Gln Leu Gly Arg Glu Ile Asp Asp His Asp Ala Val
 195 200 205

 Leu Arg Phe Asn Gly Ala Pro Thr Ala Asn Phe Gln Gln Asp Val Gly
 210 215 220

 Thr Lys Thr Thr Ile Arg Leu Met Asn Ser Gln Leu Val Thr Thr Glu
 225 230 235 240

 Lys Arg Phe Leu Lys Asp Ser Leu Tyr Asn Glu Gly Ile Leu Ile Val
 245 250 255

 Trp Asp Pro Ser Val Tyr His Ser Asp Ile Pro Lys Trp Tyr Gln Asn
 260 265 270

 Pro Asp Tyr Asn Phe Phe Asn Asn Tyr Lys Thr Tyr Arg Lys Leu His
 275 280 285

 Pro Asn Gln Pro Phe Tyr Ile Leu Lys Pro Gln Met Pro Trp Glu Leu
 290 295 300

 Trp Asp Ile Leu Gln Glu Ile Ser Pro Glu Glu Ile Gln Pro Asn Pro
 305 310 315 320

 Pro Ser Ser Gly Met Leu Gly Ile Ile Ile Met Met Thr Leu Cys Asp
 325 330 335

 Gln Val Asp Ile Tyr Glu Phe Leu Pro Ser Lys Arg Lys Thr Asp Val
 340 345 350

 Cys Tyr Tyr Tyr Gln Lys Phe Phe Asp Ser Ala Cys Thr Met Gly Ala
 355 360 365

 Tyr His Pro Leu Leu Tyr Glu Lys Asn Leu Val Lys His Leu Asn Gln
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 Gly Thr Asp Glu Asp Ile Tyr Leu Leu Gly Lys Ala Thr Leu Pro Gly
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 Phe Arg Thr Ile His Cys
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ggg aac gtc tct tcc aaa atg ctg aac ccg cgc ctg cag aag gcg atg Gly Asn Val Ser Ser Lys Met Leu Asn Pro Arg Leu Gln Lys Ala Met	210	215	220	225	850
aag gat tac ctg acc gcc aac aag cac ggg gtg cgc ttc cgc ggg aag Lys Asp Tyr Leu Thr Ala Asn Lys His Gly Val Arg Phe Arg Gly Lys		230	235	240	898
cg ^g gag gcc ggg ctg agc agg gca cag ctg ctg tgc cag ctg cgg agc Arg Glu Ala Gly Leu Ser Arg Ala Gln Leu Leu Cys Gln Leu Arg Ser		245	250	255	946
cgc g ^g g ^g cgc gtg cgg acg ctg gac ggc acc gag g ^g ccc ttt tct g ^g Arg Ala Arg Val Arg Thr Leu Asp Gly Thr Glu Ala Pro Phe Ser Ala		260	265	270	994
ctg g ^g g ^g tgg cg ^g cgc ctg gtg ccc gcc gtg ccc ctg agc cag ctg cac Leu Gly Trp Arg Arg Leu Val Pro Ala Val Pro Leu Ser Gln Leu His		275	280	285	1042
ccc cgc g ^g ctg cgc agc tgc gct gtc atg tct gca ggc gca atc Pro Arg Gly Leu Arg Ser Cys Ala Val Val Met Ser Ala Gly Ala Ile		290	295	300	1090
ctc aac tct tcc ttg g ^g gag gaa ata gat tct cat gat g ^g gtt ttg Leu Asn Ser Ser Leu Gly Glu Ile Asp Ser His Asp Ala Val Leu		310	315	320	1138
aga ttt aac tct gct cct aca cgt ggt tat gag aaa gat gtt ggg aat Arg Phe Asn Ser Ala Pro Thr Arg Gly Tyr Glu Lys Asp Val Gly Asn		325	330	335	1186
aaa acc acc ata cgc atc att aat tcg cag att ctg acc aac ccc agc Lys Thr Thr Ile Arg Ile Ile Asn Ser Gln Ile Leu Thr Asn Pro Ser		340	345	350	1234
cat cac ttc att gac agt tca ctg tat aaa gac gtc att ttg gtg gcc His His Phe Ile Asp Ser Ser Leu Tyr Lys Asp Val Ile Leu Val Ala		355	360	365	1282
tgg gac cct gcc cca tat tcc gca aat ctt aac ctg tgg tac aaa aaa Trp Asp Pro Ala Pro Tyr Ser Ala Asn Leu Asn Leu Trp Tyr Lys Lys		370	375	380	1330
ccg gat tac aac ctg ttc act cca tat att cag cat cgt cag aga aac Pro Asp Tyr Asn Leu Phe Thr Pro Tyr Ile Gln His Arg Gln Arg Asn		390	395	400	1378
cca aat cag cca ttt tac att ctt cat cct aaa ttt ata tgg cag ctc Pro Asn Gln Pro Phe Tyr Ile Leu His Pro Lys Phe Ile Trp Gln Leu		405	410	415	1426
tgg gat att atc cag gag aac act aaa gag aag att caa cca aac cca Trp Asp Ile Ile Gln Glu Asn Thr Lys Glu Lys Ile Gln Pro Asn Pro		420	425	430	1474

cca tct tct ggt ttc att gga atc ctc atc atg atg tcc atg tgc aga	1522
Pro Ser Ser Gly Phe Ile Gly Ile Leu Ile Met Met Ser Met Cys Arg	
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gag gtg cac gtg tat gaa tat atc cca tcc gtg cg ^g cag acg gag ctg	1570
Glu Val His Val Tyr Glu Tyr Ile Pro Ser Val Arg Gln Thr Glu Leu	
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Cys His Tyr His Glu Leu Tyr Tyr Asp Ala Ala Cys Thr Leu Gly Ala	
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Tyr His Pro Leu Leu Tyr Glu Lys Leu Leu Val Gln Arg Leu Asn Met	
485 490 495	
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Gly Thr Gln Gly Asp Leu His Arg Lys Gly Lys Val Val Leu Pro Gly	
500 505 510	
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Phe Gln Ala Val His Cys Pro Ala Pro Ser Pro Val Ile Pro His Ser	
515 520 525	
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